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Sequence Listing was accepted.

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Reviewer: markspencer

Timestamp: Thu Jul 12 15:27:39 EDT 2007

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Application No: 10522366 Version No: 2.0

Input Set:

Output Set:

Started: 2007-07-06 15:28:44.369  
Finished: 2007-07-06 15:28:45.210  
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 841 ms  
Total Warnings: 13  
Total Errors: 0  
No. of SeqIDs Defined: 24  
Actual SeqID Count: 24

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (2)
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W 213	Artificial or Unknown found in <213> in SEQ ID (4)
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W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (21)
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# SEQUENCE LISTING

<110> MACHIDA, Masayuki  
MASAKI, Haruhiko  
KUNIHIRO, Sumiko  
HAGIWARA, Hiroko

<120> MARKER FOR SELECTING TRANSFORMANT WITH THE USE OF LETHAL GENE

<130> 040894-7170-US

<140> 10522366

<141> 2007-07-06

<150> US 10/522,366

<151> 2005-01-25

<150> PCT/JP03/09543

<151> 2003-07-28

<150> JP 2002-218735

<151> 2002-07-26

<160> 24

<170> PatentIn version 3.4

<210> 1

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cagaatggtg gtggaaaacg caagcgctgg actggagata aagggcgtaa gatttatgag 180

tgggattctc agcatggtga gcttgagggg tatcgtgccg gtgatggtca gcatcttggc 240

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<400> 9  
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aaggataatg ttaataacgg ttgctttgat gttatagctg aatgggtacc tttgctacaa 180  
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tatccctcct gatcttctaaa aaattttcca cctgaacttg acagaaaaaa cgatgacgag 240  
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 <212> PRT  
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<400> 17

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 20 25 30

Ala Ser Asp Gly Ser Gly Trp Ser Ser Glu Asn Asn Pro Trp Gly Gly  
 35 40 45

Gly Ser Gly Ser Gly Ile His Trp Gly Gly Gly Ser Gly His Gly Asn  
 50 55 60

Gly Gly Gly Asn Gly Asn Ser Gly Gly Gly Ser Gly Thr Gly Gly Asn  
 65 70 75 80

Leu Ser Ala Val Ala Ala Pro Val Ala Phe Gly Phe Pro Ala Leu Ser  
 85 90 95

Thr Pro Gly Ala Gly Gly Leu Ala Val Ser Ile Ser Ala Gly Ala Leu  
 100 105 110

Ser Ala Ala Ile Ala Asp Ile Met Ala Ala Leu Lys Gly Pro Phe Lys  
 115 120 125

Phe Gly Leu Trp Gly Val Ala Leu Tyr Gly Val Leu Pro Ser Gln Ile  
 130 135 140

Ala Lys Asp Asp Pro Asn Met Met Ser Lys Ile Val Thr Ser Leu Pro  
 145 150 155 160

Ala Asp Asp Ile Thr Glu Ser Pro Val Ser Ser Leu Pro Leu Asp Lys  
165 170 175

Ala Thr Val Asn Val Asn Val Arg Val Val Asp Asp Val Lys Asp Glu  
180 185 190

Arg Gln Asn Ile Ser Val Val Ser Gly Val Pro Met Ser Val Pro Val  
195 200 205

Val Asp Ala Lys Pro Thr Glu Arg Pro Gly Val Phe Thr Ala Ser Ile  
210 215 220

Pro Gly Ala Pro Val Leu Asn Ile Ser Val Asn Asn Ser Thr Pro Ala  
225 230 235 240

Val Gln Thr Leu Ser Pro Gly Val Thr Asn Asn Thr Asp Lys Asp Val  
245 250 255

Arg Pro Ala Gly Phe Thr Gln Gly Gly Asn Thr Arg Asp Ala Val Ile  
260 265 270

Arg Phe Pro Lys Asp Ser Gly His Asn Ala Val Tyr Val Ser Val Ser  
275 280 285

Asp Val Leu Ser Pro Asp Gln Val Lys Gln Arg Gln Asp Glu Glu Asn  
290 295 300

Arg Arg Gln Gln Glu Trp Asp Ala Thr His Pro Val Glu Ala Ala Glu  
305 310 315 320

Arg Asn Tyr Glu Arg Ala Arg Ala Glu Leu Asn Gln Ala Asn Glu Asp  
325 330 335

Val Ala Arg Asn Gln Glu Arg Gln Ala Lys Ala Val Gln Val Tyr Asn  
340 345 350

Ser Arg Lys Ser Glu Leu Asp Ala Ala Asn Lys Thr Leu Ala Asp Ala  
355 360 365

Ile Ala Glu Ile Lys Gln Phe Asn Arg Phe Ala His Asp Pro Met Ala  
370 375 380

Gly Gly His Arg Met Trp Gln Met Ala Gly Leu Lys Ala Gln Arg Ala

385 390 395 400

Gln Thr Asp Val Asn Asn Lys Gln Ala Ala Phe Asp Ala Ala Ala Lys  
405 410 415

Glu Lys Ser Asp Ala Asp Ala Ala Leu Ser Ser Ala Met Glu Ser Arg  
420 425 430

Lys Lys Lys Glu Asp Lys Lys Arg Ser Ala Glu Asn Asn Leu Asn Asp  
435 440 445

Glu Lys Asn Lys Pro Arg Lys Gly Phe Lys Asp Tyr Gly His Asp Tyr  
450 455 460

His Pro Ala Pro Lys Thr Glu Asn Ile Lys Gly Leu Gly Asp Leu Lys  
465 470 475 480

Pro Gly Ile Pro Lys Thr Pro Lys Gln Asn Gly Gly Gly Lys Arg Lys  
485 490 495

Arg Trp Thr Gly Asp Lys Gly Arg Lys Ile Tyr Glu Trp Asp Ser Gln  
500 505 510

His Gly Glu Leu Glu Gly Tyr Arg Ala Ser Asp Gly Gln His Leu Gly  
515 520 525

Ser Phe Asp Pro Lys Thr Gly Asn Gln Leu Lys Gly Pro Asp Pro Lys  
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Arg Asn Ile Lys Lys Tyr Leu  
545 550

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<212> PRT  
<213> Escherichia coli

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20 25 30

Lys Gly Leu Gly Asp Leu Lys Pro Gly Ile Pro Lys Thr Pro Lys Gln  
35 40 45

Asn Gly Gly Gly Lys Arg Lys Arg Trp Thr Gly Asp Lys Gly Arg Lys  
50 55 60

Ile Tyr Glu Trp Asp Ser Gln His Gly Glu Leu Glu Gly Tyr Arg Ala  
65 70 75 80

Ser Asp Gly Gln His Leu Gly Ser Phe Asp Pro Lys Thr Gly Asn Gln  
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Leu Lys Gly Pro Asp Pro Lys Arg Asn Ile Lys Lys Tyr Leu  
100 105 110

<210> 19  
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<212> PRT  
<213> Escherichia coli

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Glu Asn Ile Lys Gly Leu Gly Asp Leu Lys Pro Gly Ile Pro Lys Thr  
20 25 30

Pro Lys Gln Asn Gly Gly Gly Lys Arg Lys Arg Trp Thr Gly Asp Lys  
35 40 45

Gly Arg Lys Ile Tyr Glu Trp Asp Ser Gln His Gly Glu Leu Glu Gly  
50 55 60

Tyr Arg Ala Ser Asp Gly Gln His Leu Gly Ser Phe Asp Pro Lys Thr  
65 70 75 80

Gly Asn Gln Leu Lys Gly Pro Asp Pro Lys Arg Asn Ile Lys Lys Tyr  
85 90 95

Leu

<210> 20

<211> 330  
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 <213> *Escherichia coli*

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 caaagcagaa tgggtggtgga aaacgcaagc gctggactgg agataaaggg cgtaagattt 180  
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 <223> Synthetic single-stranded oligonucleotide

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 <213> *Saccharomyces cerevisiae*

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 gctactctcc caaaacaaa aggtctccgc tgactagggc acatctgaca gaagtggaat 180  
 caaggctaga aagactggaa cagctatttc tactgatttt tcctcgagaa gaccttgaca 240  
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ctctaacatt gagacagcat agaataagtg cgacatcatc atcgaagag agtagtaaca	420
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 <213> *Aspergillus oryzae*

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